Figure 1

DSP-12, 1656 Base Pairs

```
AAGCAGTGGTAACAACGCAGAGTACGCGGGCGAGGAGAATATCTTGCTGGGAGTGGACT
TTTCCAGTAAGGAAAGTAAAAGCTGCACCATTGGGATGGTTCTCCGACTGTGGAGCGAC
ACGAAAATCCATCTTGATGGAGATGGTTGGTTCAGCCTGAGCACAGCAGGAAGGATGCA
CATATTTTAGCCTCTCTCTGTCCAACAGCACGTGTCTCCCCCCGCACCTTGCTTCACAAGG
CCTGCGAAGTGGCCCGGAGGCACAACTACTTCCCCGGGGGTGTAGCTCTCATCTGGGCT
ACCTACTATGAGAGCTGCATCAGCTCCGAGCAGAGCTGCATCAACGAGTGGAACGCCAT
GCAGGACCTGGAGTCTACGCGGCCCGACTCCCCCGCGCTATTTGTGGACAAGCCCACTG
AAGGGGAAAGGACCGAGCGGCTCATCAAAGCCAAGCTCCGAAGCATCATGATGAGCCAG
GATCTAGAAAATGTGACTTCCAAAGAGATTCGTAATCATTTACAGAAACAGATGAATTG
TAACTTGAAGGAACTCAAGGAATTTATAGACAATGAGATGCTACTTATCTTGGGACAGA
TGGACAAGCCCTCCCTTATCTTCGATCATCTTTATCTCGGCTCTGAATGGAATGCATCC
AATCTGGAGGAACTGCAGGGCTCAGGGGTTGATTACATTTTAAATGTTACCAGAGAAAT
CGATAATTTTTTTCCTGGCTTATTTGCATACCATAACATCCGAGTCTACGATGAAGAGA
CCACAGACCTCCTCGCCCACTGGAATGAAGGCTATCATTTTATAAAACAAAGCGAAGAGG
AACCATTCCAAGTGCCTGGTGCATTGCAGAATGGGCGTGAGTCGGTCGGCCTCCACAGT
CATAGCCTATGCAATGAAGGAATTCGGCTGGCCTCTGGAAAAAGCATATAACTATGTAA
AGCAGAAGCGCAGCATCACGCGGCCCAACGGCGGCTTTATGAGGCAGCTGTCTGAGTAT
GAAGGCATCTTGGATGCAAGCAAACAGCCGGCACAACAAGCTGTGGCGTCAGCAGACAGA
CAGCAGCCTCCAGCAGCCTGTGGATGACCCTGCAGGACCTGGCGACTTCTTGCCAGAGA
CCCCAGATGGCACCCCGGAAAGCCAGCTGCCCTTCTTGGATGATGCCGCCCAGCCCGGC
TTAGGGCCCCCCCTCCCCTGCTGTTTCCGGCGACTCTCAGACCCCCTTCTGCCTTCCCC
TGAGGATGAAGCCGGCAGCTTGGTCCACCTGGAGGATCCGGAGAGGGGAGGCTCTGTTGG
AGGAAGCTGCTCCACCTGCAGAGGTGCACAGGCCGGCCAGACAGCCCCAGCAAGGTTCC
GGACTCTGTGAGAAGGATGTGAAGAAGAAACTAGAGTTTGGGAGTCCCAAAGGTCGGAG
CGGCTCCTTGCTGCAGGTGGAGGAGACGGAAAGGGAGGAGGGCCTGGGAGCAGGGAGGT
GGGGGCAGCTTCCAACCCAGCTCGATCAAAACCTGCTCAACTCGGAGAACCTAAACAAC
AACATTAACATAATCTTTTTCAAAGTATGCAAGTATTCAGAGCCCGGCCTGCATGGTG
GCACACACGCACCTTTCATCCCACTTTAATTACGCTATCTTCAGTTTCTGTAGTAGGGA
CTACAACGACTTTCTACACCAGCAATTCAATTTTTTCTATTCTCTTTCCTCTCCCCCC
AGCTCTTATCTTCAGTCACCTGACGGTTCTTTCACAGCCTGATTCTCGTCGGCCGGTACC
TAGTGCATACCTTATATAGGCAAATTGAGAATCTGTTGGGAATAACACATATCTCTGCAC
ACCATCTTCATGCCATGTACCTTATTCATACCCTGGCAGGGGTTCCCCACTCAATTTCT
TTTCTGTATCTAAAATTAAAAACATATAATTTATGAGCCAAAAAAAAAAAAAAAAAAAA
AA
```

Figure 2

DSP-12, 552 Amino Acids

```
MVLRLWSDTKIHLDGDGGFSVSTAGRMHIFKPVSVQAMWSALQVLHKACEVARRHNYFP
GGVALIWATYYESCISSEQSCINEWNAMQDLESTRPDSPALFVDKPTEGERTERLIKAK
LRSIMMSQDLENVTSKEIRNELEKQMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLY
LGSEWNASNLEELQGSVETILNVIAEIGNFFGLFAYHNIRVIDEEITDLLAHWNEAY
HFINKAKRNHSKCLVHCKMGVSRSASTVIAYAMKEFGWPLEKAYNYVKQKRSITRPNAG
FMRQLSEYEGILDASKQRHNKLWRQQTDSSLQQPVDDPAGPGDFLPETPDGTPESQLPF
LDDAAQPGLGPPLPCCFRRLSDPLLPSPEDEAGSLVHLEDPEREALLEEAAPPAEVHRP
ARQPQQGSGLCEKDVKKKLEFGSPKGRSGSLLQVEETEREEGLGAGRWGQLPTQLDQNL
LNSENLNNNSKRSCPNGMEVGRARPAGWHTPSLPSHSNWPTSASVVGTTGTRHHTQLIF
FYCLLWAPSSHLQGPEGSFTG
```

Figure 3

DSP-13, 1527 Base Pairs

```
CCTGGGAAGAAGTTATCTATCTCTCGAGTGACATTCAAGATATACCGTACCCCTCGGTTCTGTA
AGTCCTCTAAGTTGGAGGCATTCCATTCTGAGCCGGCCCCATGACCCTGAGCACGTTGGCCCGC
AAGAGGAAGGCGCCCCTCGCTTGCACCTGCAGCCTCGGTGGCCCCGACATGATTCCTTACTTCT
CCGCCAACGCGGTCATCTCGGCAGAACGGCCATCAACCAGCTCATCAGCCGAGCCTTTCTAACTGT
CAAAGGTGCTGCCCTTTTTCTACCACGGGGAAATGGCTCATCCACACCAAGAATCAGCCACAGA
CCGGAACAAGCATGCAGGCGATCTCCAACAGCATCTCCAAGCAATGTTCATTTTACTCCGCCCAG
AAGACAACATCAGGCTGGCTGTAAGACTGGAAAGTACTTACCAGAATCGAACACGCTATATGGT
AGTGGTTTCAACTAATGGTAGACAAGACACTGAAGAAAGCATCGTCCTAGGAATGGATTTCTCC
TCTAATGACAGTAGCACTTGTACCATGGGCTTACTTTTCCCTCTCTGGAGCGACACGCTAATTC
ATTTGGATGGTGATGGTGGGTTCAGTGTATCGACGGATAACAGAGTTCACATATTCAAACCTGT
ATCTGTGCAGGCAATGTGGTCTGCACTACAGAGCTTACACAAGGCTTGTGAAGTCGCCAGAGCG
CATAACTACTACCAGGCAGCCTATTTCTCACTTGGGTGAGTTATTATGAGAGCCATATCAACT
CAGATCAATCCTCAGTCAATGAATGGAATGCAATGCAAGATGTACAGTCCCACCGGCCCGACTC
TCCAGCTCTCTTCACCGACATACCTACTGAACGTGAACGAACAGAAAGGCTAATTAAAACCAAA
TTAAGGGAGATCATGATGCAGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGT
TGGAAATGCAAATGGTGTGCAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGT
GATCCTTGGTCAAATGGATAGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGG
AATGCCTCCAACTTAGAGGACTTACAGAACCGAGGGGTACGGTATATCTTGAATGTCACTCGAG
AGATAGATAACTTCTTCCCAGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGC
AACGGATCTCCTGGCGTACTGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGA
TCTAAATGCCTTGTGCACTGCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATG
CAATGAAGGAATATGGCTGGAATCTGGACCGAGCCTATGACTATGTGAAAGAAAGACGAACGGT
AACCAAGCCCAACCCAAGCTTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGC
TTCCTAGGCTTGATTCATGGAGGGAGGACAAGCCCTGGGGAGAGAAAGCACAGAATTTGAGT
CAGTAGATCTGGTTTCCATTCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACAT
TTCTCATCCTTACCTGACCCCATCTATAAAATGAAAATCAAGAGATCCATCTCACAGGGTTATT
GTCAATAAAAATGTGTTTGAATTTTTATAAAAAAAAAAAAAAAAAA
```

Figure 4

DSP-13, 509 Amino Acids

```
MTLSTLARKRKAPLACTCSLGGPDMIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGS
STPRISHRRNKHAGDLQQHLQAMFILLRPEDNIRLAVRLESTYQNRTRYMVVVSTNGRQDTEES
IVLGMDFSSNDSSTCTMGLVLPLWSDTLIHLDGDGGFSVSTDNRVHIFKPVSVQAMWSALQSLH
KACEVARAHSYPGSLFLIWLSYYESHINSDQSSVNEWNAMQDVQSHRPDSPALFTDIPTERER
TERLIKTKLREIMMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFE
HVFLGSEWNASNLEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKF
ISKAKKHGSKCL**VHCKMGVSRS**ASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEE
YQGILLASFLGLIHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK
```

Figure 5

A   DSP13 Alternate Splice Variant, 723 Base Pairs

```
CTGCCCGGCTTCTAACAGGCCACTGACCGGTACTCACTGGGGACCCACGCTCTAAGTTGTTGAT
CTCTAGAACCGATTTTGGAAAAGGATTTGCCTTATTGAAGAAGACAGGATCATTCTTCTTTCTT
TCCCATTTAAGAATAATCGTTATTAAGAATATCGTTAAGAATAATCGTTATTTCTCTCTTCTC
AGACCTACTGAACGTGAACGAACAGAAAGGCTAATTAAAACCAAATTAAGGGACATCATGATGC
AGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGTTGGAAATGCAAATGGTGTG
CAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGTGATCCTTGGTCAAATGGAT
AGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGGAATGCCTCCAACTTAGAGG
ACTTACAGAACCGAGGGGGTACGGTATATCTTGAATGTCACTCGAGAGATAGATAACTTCTTCCC
AGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGCCAACCCATCTCCTGGCGTAC
TGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGATCTAAATGCCTTGTGCACT
GCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATGCAATGAAGGAATATGGCTG
GAATCTGGACCGAGCCTATGACTATGTGAAAGAAAGACGAACGGTAACCAAGCCCAACCCAAGC
TTCATGAGACAACTGGAAGAGTATCAGGGGGATCTTGCTGGCAAGCTTCCTAGGCTTGATTCATG
GAGGGAGGGACAAGCCCTGGGGAGAGAAAAGCACAGAATTTGAGTCAGTAGATCTGGTTTCCAT
TCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACATTTCTCATCCTTACCTGACC
CCATCTATAAAATGAAAATCAAGAGATCCATCTCACAGGGTTATTGTGAATAAAAATGTGTTTG
AATGTTTATAAAAAAAAAAAAAAAAAAAAAA
```

B   DSP13 Alternate Splice Variant, 241 Amino Acids

```
MMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFEHVFLGSEWNASN
LEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKFISKAKKHGSKCL
VHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEEYQGILLASFLGL
```

```
        10         20         30         40         50         60         70         80         90        100
1 -------+----------+----------+----------+----------+----------+----------+----------+----------+----------+
SOLQRD-PNSATDSDGSPLSNSQPSFPVEILPFLYLGCAKDSTNLDVLEEFGIKYILNVTP----------NLPNLFENAGEFKYKQIPISDHWSQNLSQF
DREIPSSAILSDGSPVPSSQPAFPVQILPYLYLGCAKDSTNLDVLGKYGIKYILNVTP----------NIPNMFENGGEFTYKQIPISDHWSQNLSQF
GATPPPVGLRHSFPVQILPNLYLGSARDSANLESLAKLGIRYILNVTP----------NLPNIFFEKNGDFHYKQIPISDHWSQNLSRF
GLCEGKPAALLPHSLSQPCLPVPSVGLTRILPHLYLGSQKDVLNKDLMTQNGISYVLNASN----------SCPKP-DFICESRFHRVPINDNYCEKLLPH
PAQALPPAGAENSNSDPRVPIYDQGGPVEILPYLYLGSCNHSSDLQGLQACGITAVLNVSH----------SCPNHFE--GLFHYKSIPVEDNQMVEISAH
PLSTSVPDSAESGCSSCSTPLYDQGGPVEILPFLYLGSAYHASRKDMLDALGITALINVSH----------NCPNHFE--GHYQYKSIPVEDNHKADISSH
PVPPSATEPLDLGCSSCGTPLHDQGGPVEILPFLYLGSAYHARRDMLDALGITALLNVSS----------DCPNHFE--GHYQYKCIPVEDNHKADISSH
SERALISQCGKPVVNVSYRPAYDQGGPVEILPFLYLGSAYHASKCEFLANLHITALLNVSR----------RTSEARCM--THLHYKAIPVEDSHTADISSH
QMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLYLGSEWNASNLEELQGSGVDYILNVTR----------EIDNFFP--GLFAYHNIRVYDEETTDLLAH
QMVCNLREFKEFIDNEHIVILGQMDSPTQIFEHVFLGSEWNASNLEDLQNRGVRYILNVTR----------EIDNFF9.--GVFEYHNIRVYDEEATDLLAY
SGSFELSVQDLNDILSDGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLMAAEGRSFHHVNTKHNFYKDSGITYLGIKANDTQEFNLSAY
                    P e!lp lYlGsa      a u   $     g! y LNu        pn f     g  %  !p  0   ls

        110        120        130        140        150        160        170       182
101 ----+----------+----------+----------+----------+----------+----------+----------+
FPEAISFIDEA-RGKNCGVLVHCLAGISRSVTVTVAYLMQKLNLSMNDAYDIVKHKKSNISPNFNFMGQLLDFERTLGLSS
FPEAISFIDEA-RSKKCGVLVHCLAGISRSVTVTVAYLMQKLNLSLNDAYDFVKRKKSNISPNFNFMGQLLDFERTLGLSS
FPEAIEFIDEA-LSQNCGVLVHCLAGVSRSVTVTVAYLMQKLHLSLNDAYDLVKRKKSNISPNFNFMGQLLDFERSLRLE
LDKSIEFIDKA-KLSSCQVIVHCLAGISRSATIAIAYIMKTMGHSSDDAYRFVKDRRPSISPNFNFLGQLLEYERTLKLLA
FQEAISFIDSV-KNSGGRVLVHCQAGISRSATICLAYLIQSHRVRLDEAFDFVKQRRGVISPNFSFMGQLLQLTQVLCH
FNEAIDFIDSI-KNAGGRVFVHCQAGISRSATICLAYLMRTNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAPH
FMEAIEYIDAV-KDCRGRVLVHCQAGISRSATICLAYLMHKKRVRLEFAFEFVKQRRSIISPNFSFMGQLLQFESQVLATS
FQEAIDFIDCV-REKGGKVLVHCEAGISRSPTICMAYLHKTKQFRLKEAFDYIKQRRSMYSPNFGFMGQLLQYESEILPSTP
WNEAYHFINKA-KRNIISKCLVHCKMGVSRSASTVIAYAMKEFGAPLEKAYNYVKQKRSIITKPNAGFMRQLSEYFGIIDASKQ
WNDTYKFISKA-KHIGSKCLVHCKMGVSRSASTVIAYAMKEYGANLDRAYDYVKERRTVTKPNPSFMRQLEEYQGIILASFL
FFRAADFIDVALAQKNGRVLVHCREGYSRSPTLVIAYLHHRQKHDVKSALSIVRQNRE-IGPNDGFLAQLCQLNDRLAKEG
f eai FI# a k   vlVHC aGiSRSat iAYlH      l  Ay !kqrr isPNf F$gQLl# # l
```

Figure 6

Alignment of DSP-12 and DSP-13

```
           10        20        30        40        50        60        70        80        90       100       110
1   ---+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----
    MILSILARKRKAPLACICSIGGPDHIPYFSNAVISQNAINQLIGESFLIVKGAALFLPRGNGSSIPRISHRRNKINGDLQQNLQAMEILLRPEDNIRLAVRLESIYQNR

          120       130       140       150       160       170       180       190       200       210       220
111 ---+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----
                                         MVLRLASDIKIHLDGDGGFSVSINGRMIIFKPYSVQNMSALQVLIKACIVIARRINYFPGGVNLIANIYYESCI
    IRYHVVSINGRQDIIFSIYHGMDFSSNDSSICIHGLVLPLASDILIHLDGDGGFSVSIDNRVIIIFKPYSVQNMSALQSIIKACIVIRIHNYYPGGSLFLIAVSYYFSHI

          230       240       250       260       270       280       290       300       310       320       330
221 ---+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----
    SSEQSCINEHNAMQDESIRPDSPALFVDKPIEGERIERLIKAKLRSIHHSQDLENVISKEIRNELEKDHHCNLKELKEFIDNEMLIIGDMDKPSLIFDHLYLGSEARH
    NSDQSSVNEHNAMQHKQSHRPDSPALFIDIPIERERIERLIKIKLRLEIHHQKDLENIISKEIRIELEMQMVCNLRLFKEFIDNEMIVILGQHDSPIQIFEHVILGSEHNH

          340       350       360       370       380       390       400       410       420       430       440
331 ---+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----
    SNLEELQGSGVDYIIGVIREIDNFFPGLEAYINIRYDEEIIDLLAHHHEDYIIFINKAKRNISKCLVHCKHGVSRSASIVIAYAHKFIGHPLEKAYNYVKQKRSIIRPHH
    SNLEDLQNRGVRYIIGVIREIDNFFPGVFEYINIRYDEEIIDLLAYHHDIYKFISKAKKHGSKCLVHCKHGVSRSASIVIAYAHKEYGHNLQRAYDYVKIERIVIKPNP

          450       460       470       480       490       500       510       520       530       540       550
441 ---+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----
    GIMRQLSEYIGIIDESKQR---HHKLARQQTDSSLQ-QPYDDPAGPGDFLPEIPDGIPESQLPEFLDDAFQPGLGPPLPCCFRRLSDPLLPSPEDEAGSLVHLLDPIREALL
    SIMRQLFYQGIIDSFIGIIHGGRDKPHGEKSIEFESVDLYSIPGSISPSCCHPEKLLHISHPYLIPSIK

          560       570       580       590       600       610       620       630       640       650       660
551 ---+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----
    EEHAPPHEVHRPHRGPQQGSGICEKDYKKKLEFGSPKGKRSGSLIGVEFIERIEGLGAGRHGQLPTQLDQNLLNSEHLNNNSKRSCPHGHEVGRARPAGHHIPSLPSHSNH

          670       680       690       701
661 ---+----+----+----+----+----+----+----+
    PISHSVVGIIGIRHHIIQLIFFYCLLHAPSSHLQGPEGSFIG
```

Figure 7